

R. Mitra

# 8

RSL Entered - 1653  
7/5/01

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/523,647

DATE: 07/05/2001

TIME: 11:21:32

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Output Set: N:\CRF3\07052001\I523647.raw

3 <110> APPLICANT: MURDIN, ANDREW D.  
 4 OOMEN, RAYMOND P.  
 5 WANG, JOE  
 6 DUNN, PAMELA  
 8 <120> TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING  
 9 DNA FRAGMENTS AND USES THEREOF  
 11 <130> FILE REFERENCE: 032931/0227  
 13 <140> CURRENT APPLICATION NUMBER: 09/523,647  
 C--> 14 <141> CURRENT FILING DATE: 2000-03-10  
 16 <150> PRIOR APPLICATION NUMBER: 60/123,966  
 17 <151> PRIOR FILING DATE: 1999-03-12  
 19 <160> NUMBER OF SEQ ID NOS: 4  
 21 <170> SOFTWARE: PatentIn Ver. 2.1  
 23 <210> SEQ ID NO: 1  
 24 <211> LENGTH: 2111  
 25 <212> TYPE: DNA  
 26 <213> ORGANISM: Chlamydia pneumoniae  
 28 <220> FEATURE:  
 29 <221> NAME/KEY: CDS  
 30 <222> LOCATION: (139)..(1809)  
 32 <400> SEQUENCE: 1  
 33 ttgatcaggt agttaggaga tgaattaatt cctgactacc ttaattcaga taataaaccc 60  
 35 aaatgttgag ggtaagagtt tacaaaacat tctaccgat ggcagaagaa aaaaataaac 120  
 37 atgcgatagg agatccct atg tcc aaa ctc atc aga cga gta gtt acg gtc 171  
 38 Met Ser Lys Leu Ile Arg Arg Val Val Thr Val  
 39 1 5 10  
 41 ctt gcg cta acg agt atg gcg agt tgc ttt gcc agc ggg ggt ata gag 219  
 42 Leu Ala Leu Thr Ser Met Ala Ser Cys Phe Ala Ser Gly Gly Ile Glu  
 43 15 20 25  
 45 gcc gct gta gca gag tct ctg att act aag atc gtc gct agt gcg gaa 267  
 46 Ala Ala Val Ala Glu Ser Leu Ile Thr Lys Ile Val Ala Ser Ala Glu  
 47 30 35 40  
 49 aca aag cca gca cct gtt cct atg aca gcg aag aag gtt aga ctt gtc 315  
 50 Thr Lys Pro Ala Pro Val Pro Met Thr Ala Lys Lys Val Arg Leu Val  
 51 45 50 55  
 53 cgt aga aat aaa caa cca gtt gaa caa aaa agc cgt ggt gct ttt tgt 363  
 54 Arg Arg Asn Lys Gln Pro Val Glu Gln Lys Ser Arg Gly Ala Phe Cys  
 55 60 65 70 75  
 57 gat aaa gaa ttt tat ccc tgt gaa gag gga cga tgt caa cct gta gag 411  
 58 Asp Lys Glu Phe Tyr Pro Cys Glu Glu Gly Arg Cys Gln Pro Val Glu  
 59 80 85 90  
 61 gct cag caa gag tct tgc tac gga aga ttg tat tct gta aaa gta aac 459  
 62 Ala Gln Gln Glu Ser Cys Tyr Gly Arg Leu Tyr Ser Val Lys Val Asn  
 63 95 100 105  
 65 gat gat tgc aac gta gaa att tgc cag tcc gtt cca gaa tac gct act 507  
 66 Asp Asp Cys Asn Val Glu Ile Cys Gln Ser Val Pro Glu Tyr Ala Thr  
 67 110 115 120

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69 gta gga tct cct tac cct att gaa atc ctt gct ata ggc aaa aaa gat 555
70 Val Gly Ser Pro Tyr Pro Ile Glu Ile Leu Ala Ile Gly Lys Lys Asp
71      125      130      135
73 tgt gtt gat gtt gtg att aca caa cag cta cct tgc gaa gct gaa ttc 603
74 Cys Val Asp Val Val Ile Thr Gln Gln Leu Pro Cys Glu Ala Glu Phe
75 140      145      150      155
77 gta agc agt gat cca gaa aca act cct aca agt gat ggg aaa tta gtc 651
78 Val Ser Ser Asp Pro Glu Thr Thr Pro Thr Ser Asp Gly Lys Leu Val
79      160      165      170
81 tgg aaa atc gat cgc ctg ggt gca gga gat aaa tgc aaa att act gta 699
82 Trp Lys Ile Asp Arg Leu Gly Ala Gly Asp Lys Cys Lys Ile Thr Val
83      175      180      185
85 tgg gta aaa cct ctt aaa gaa ggt tgc tgc ttc aca gct gct act gta 747
86 Trp Val Lys Pro Leu Lys Glu Gly Cys Cys Phe Thr Ala Ala Thr Val
87      190      195      200
89 tgt gct tgc cca gag ctc cgt tct tat act aaa tgc ggt caa cca gcc 795
90 Cys Ala Cys Pro Glu Leu Arg Ser Tyr Thr Lys Cys Gly Gln Pro Ala
91      205      210      215
93 att tgt att aag caa gaa gga cct gac tgt gct tgc cta aga tgc cct 843
94 Ile Cys Ile Lys Gln Glu Gly Pro Asp Cys Ala Cys Leu Arg Cys Pro
95 220      225      230      235
97 gta tgc tac aaa atc gaa gta gtg aac aca gga tct gct att gcc cgt 891
98 Val Cys Tyr Lys Ile Glu Val Val Asn Thr Gly Ser Ala Ile Ala Arg
99      240      245      250
101 aac gta act gta gat aat cct gtt ccc gat ggc tat tct cat gca tct 939
102 Asn Val Thr Val Asp Asn Pro Val Pro Asp Gly Tyr Ser His Ala Ser
103      255      260      265
105 ggt caa aga gtt ctc tct ttt aac tta gga gac atg aga cct ggc gat 987
106 Gly Gln Arg Val Leu Ser Phe Asn Leu Gly Asp Met Arg Pro Gly Asp
107      270      275      280
109 aaa aag gta ttt aca gtt gag ttc tgc cct caa aga aga ggt caa atc 1035
110 Lys Lys Val Phe Thr Val Glu Phe Cys Pro Gln Arg Arg Gly Gln Ile
111      285      290      295
113 act aac gtt gct act gta act tac tgc ggt gga cac aaa tgt tct gca 1083
114 Thr Asn Val Ala Thr Val Thr Tyr Cys Gly Gly His Lys Cys Ser Ala
115 300      305      310      315
117 aat gta act aca gtt gtt aat gag cct tgt gta caa gta aat atc tct 1131
118 Asn Val Thr Thr Val Val Asn Glu Pro Cys Val Gln Val Asn Ile Ser
119      320      325      330
121 ggt gct gat tgg tct tac gta tgt aaa cct gtg gag tac tct atc tca 1179
122 Gly Ala Asp Trp Ser Tyr Val Cys Lys Pro Val Glu Tyr Ser Ile Ser
123      335      340      345
125 gta tcg aat cct gga gac ttg gtt ctt cat gat gtc gtg atc caa gat 1227
126 Val Ser Asn Pro Gly Asp Leu Val Leu His Asp Val Val Ile Gln Asp
127      350      355      360
129 aca ctc cct tct ggt gtt aca gta ctc gaa gct cct ggt gga gag atc 1275
130 Thr Leu Pro Ser Gly Val Thr Val Leu Glu Ala Pro Gly Gly Glu Ile
131      365      370      375
133 tgc tgt aat aaa gtt gtt tgg cgt att aaa gaa atg tgc cca gga gaa 1323

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134 Cys Cys Asn Lys Val Val Trp Arg Ile Lys Glu Met Cys Pro Gly Glu
135 380 385 390 395
137 acc ctc cag ttt aaa ctt gta gtg aaa gct caa gtt cct gga aga ttc 1371
138 Thr Leu Gln Phe Lys Leu Val Val Lys Ala Gln Val Pro Gly Arg Phe
139 400 405 410
141 aca aat caa gtt gca gta act agt gag tct aac tgc gga aca tgt aca 1419
142 Thr Asn Gln Val Ala Val Thr Ser Glu Ser Asn Cys Gly Thr Cys Thr
143 415 420 425
145 tct tgc gca gaa aca aca aca cat tgg aaa ggt ctt gca gct acc cat 1467
146 Ser Cys Ala Glu Thr Thr Thr His Trp Lys Gly Leu Ala Ala Thr His
147 430 435 440
149 atg tgc gta tta gac aca aat gat cct atc tgt gta gga gaa aat act 1515
150 Met Cys Val Leu Asp Thr Asn Asp Pro Ile Cys Val Gly Glu Asn Thr
151 445 450 455
153 gtc tat cgt atc tgt gta act aac cgt ggt tct gct gaa gat act aac 1563
154 Val Tyr Arg Ile Cys Val Thr Asn Arg Gly Ser Ala Glu Asp Thr Asn
155 460 465 470 475
157 gta tct tta atc ttg aag ttc tca aaa gaa ctt cag cca ata gct tct 1611
158 Val Ser Leu Ile Leu Lys Phe Ser Lys Glu Leu Gln Pro Ile Ala Ser
159 480 485 490
161 tca ggt cca act aaa gga acg att tca ggt aat acc gtt gtt ttc gac 1659
162 Ser Gly Pro Thr Lys Gly Thr Ile Ser Gly Asn Thr Val Val Phe Asp
163 495 500 505
165 gct tta cct aaa ctc ggt tct aag gaa tct gta gag ttt tct gtt acc 1707
166 Ala Leu Pro Lys Leu Gly Ser Lys Glu Ser Val Glu Phe Ser Val Thr
167 510 515 520
169 ttg aaa ggt att gct ccc gga gat gct cgc ggc gaa gct att ctt tct 1755
170 Leu Lys Gly Ile Ala Pro Gly Asp Ala Arg Gly Glu Ala Ile Leu Ser
171 525 530 535
173 tct gat aca ctg act tca cca gta tca gac aca gaa aat acc cac gtg 1803
174 Ser Asp Thr Leu Thr Ser Pro Val Ser Asp Thr Glu Asn Thr His Val
175 540 545 550 555
177 tat taa attctaagga attatcctaa agcagagcga tattccgctc tgcttttagga 1859
178 Tyr
180 tagcttttcaa agaagtaccg ctttagtacc ttacgtacta aagcgggtttt tttgttttat 1919
182 aagctcttca atccaatcgt agagtttctt aatcaaagat attattttaag tttctgaaat 1979
184 cctaagattt attttaaaag cccatctttt taggtatgta attaaaattt ttaattaagc 2039
186 ttttcctagt gtaacctgct tcttttaggaa ctacactagg agaacggtat gtcatacaat 2099
188 ctacatcccg ta 2111
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192 <211> LENGTH: 556
193 <212> TYPE: PRT
194 <213> ORGANISM: Chlamydia pneumoniae
196 <400> SEQUENCE: 2
197 Met Ser Lys Leu Ile Arg Arg Val Val Thr Val Leu Ala Leu Thr Ser
198 1 5 10 15
200 Met Ala Ser Cys Phe Ala Ser Gly Gly Ile Glu Ala Ala Val Ala Glu
201 20 25 30
203 Ser Leu Ile Thr Lys Ile Val Ala Ser Ala Glu Thr Lys Pro Ala Pro

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204	35	40	45
206	Val Pro Met Thr Ala Lys Lys Val Arg Leu Val Arg Arg Asn Lys Gln		
207	50	55	60
209	Pro Val Glu Gln Lys Ser Arg Gly Ala Phe Cys Asp Lys Glu Phe Tyr		
210	65	70	75
212	Pro Cys Glu Glu Gly Arg Cys Gln Pro Val Glu Ala Gln Gln Glu Ser		
213	85	90	95
215	Cys Tyr Gly Arg Leu Tyr Ser Val Lys Val Asn Asp Asp Cys Asn Val		
216	100	105	110
218	Glu Ile Cys Gln Ser Val Pro Glu Tyr Ala Thr Val Gly Ser Pro Tyr		
219	115	120	125
221	Pro Ile Glu Ile Leu Ala Ile Gly Lys Lys Asp Cys Val Asp Val Val		
222	130	135	140
224	Ile Thr Gln Gln Leu Pro Cys Glu Ala Glu Phe Val Ser Ser Asp Pro		
225	145	150	155
227	Glu Thr Thr Pro Thr Ser Asp Gly Lys Leu Val Trp Lys Ile Asp Arg		
228	165	170	175
230	Leu Gly Ala Gly Asp Lys Cys Lys Ile Thr Val Trp Val Lys Pro Leu		
231	180	185	190
233	Lys Glu Gly Cys Cys Phe Thr Ala Ala Thr Val Cys Ala Cys Pro Glu		
234	195	200	205
236	Leu Arg Ser Tyr Thr Lys Cys Gly Gln Pro Ala Ile Cys Ile Lys Gln		
237	210	215	220
239	Glu Gly Pro Asp Cys Ala Cys Leu Arg Cys Pro Val Cys Tyr Lys Ile		
240	225	230	235
242	Glu Val Val Asn Thr Gly Ser Ala Ile Ala Arg Asn Val Thr Val Asp		
243	245	250	255
245	Asn Pro Val Pro Asp Gly Tyr Ser His Ala Ser Gly Gln Arg Val Leu		
246	260	265	270
248	Ser Phe Asn Leu Gly Asp Met Arg Pro Gly Asp Lys Lys Val Phe Thr		
249	275	280	285
251	Val Glu Phe Cys Pro Gln Arg Arg Gly Gln Ile Thr Asn Val Ala Thr		
252	290	295	300
254	Val Thr Tyr Cys Gly Gly His Lys Cys Ser Ala Asn Val Thr Thr Val		
255	305	310	315
257	Val Asn Glu Pro Cys Val Gln Val Asn Ile Ser Gly Ala Asp Trp Ser		
258	325	330	335
260	Tyr Val Cys Lys Pro Val Glu Tyr Ser Ile Ser Val Ser Asn Pro Gly		
261	340	345	350
263	Asp Leu Val Leu His Asp Val Val Ile Gln Asp Thr Leu Pro Ser Gly		
264	355	360	365
266	Val Thr Val Leu Glu Ala Pro Gly Gly Glu Ile Cys Cys Asn Lys Val		
267	370	375	380
269	Val Trp Arg Ile Lys Glu Met Cys Pro Gly Glu Thr Leu Gln Phe Lys		
270	385	390	395
272	Leu Val Val Lys Ala Gln Val Pro Gly Arg Phe Thr Asn Gln Val Ala		
273	405	410	415
275	Val Thr Ser Glu Ser Asn Cys Gly Thr Cys Thr Ser Cys Ala Glu Thr		
276	420	425	430

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278 Thr Thr His Trp Lys Gly Leu Ala Ala Thr His Met Cys Val Leu Asp
279           435                      440                      445
281 Thr Asn Asp Pro Ile Cys Val Gly Glu Asn Thr Val Tyr Arg Ile Cys
282           450                      455                      460
284 Val Thr Asn Arg Gly Ser Ala Glu Asp Thr Asn Val Ser Leu Ile Leu
285 465                      470                      475                      480
287 Lys Phe Ser Lys Glu Leu Gln Pro Ile Ala Ser Ser Gly Pro Thr Lys
288           485                      490                      495
290 Gly Thr Ile Ser Gly Asn Thr Val Val Phe Asp Ala Leu Pro Lys Leu
291           500                      505                      510
293 Gly Ser Lys Glu Ser Val Glu Phe Ser Val Thr Leu Lys Gly Ile Ala
294           515                      520                      525
296 Pro Gly Asp Ala Arg Gly Glu Ala Ile Leu Ser Ser Asp Thr Leu Thr
297           530                      535                      540
299 Ser Pro Val Ser Asp Thr Glu Asn Thr His Val Tyr
300 545                      550                      555
304 <210> SEQ ID NO: 3
305 <211> LENGTH: 45
306 <212> TYPE: DNA
307 <213> ORGANISM: Artificial Sequence
309 <220> FEATURE:
310 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
312 <400> SEQUENCE: 3
313 ataagaatgc ggccgccacc atgtccaaac tcatcagacg agtag                      45
316 <210> SEQ ID NO: 4
317 <211> LENGTH: 34
318 <212> TYPE: DNA
319 <213> ORGANISM: Artificial Sequence
321 <220> FEATURE:
322 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
324 <400> SEQUENCE: 4
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VERIFICATION SUMMARY

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